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MNDPNSCVDNATVCSGASC - - - VVPESNFNNILSVVLSTV ISBT
   MRA - - NC - SSSSACPANSSEEELPVGLEVHGNLELVFTVV TCH230
38 LTILLALVMFSMGCNVEIKKFLGHIKRPWGICVGFLCQFG ISBT
38 STVMMGLLMFSLGCSVEIRKLWSHIRRPWGIAVGLLCQFG TCH230
78 IMPLTGFILSVAFDILPLQAVVVLIIGCCPGGTASNILAY ISBT
78 LMPFTAYLLAISFSLKPVQAIAVLIMGCCPGGTISNIFTF TCH230
118 W V D G D M D L S V S M T T C S T L L A L G M M P L C L L I Y T K M W V D S G S ISBT
118 W V D G D M D L S I S M T T C S T V A A L G M M P L C I Y L Y T W S W S L Q Q N TCH230
158 I V I P Y D N I G T S L V A L V V P V S I G M P V N H K W P Q K A K I I L K I G ISBT
158 L T I P Y Q N I G I T L V C L T I P V A F G V Y V N Y R W P K Q S K I I L K I G TCH230
198 SIAGAILIVLIAVVGGILYQSAWIIAPKLWIIGTIFPVAG ISBT
198 AVVGGVLLLVVAVAGVVLAKGSWNSDITLLTISFIFPLIG TCH230
238 Y S LG F L L AR I A G L P W Y R C R T V A F E T G M Q N T Q L C S T I V Q L S ISBT
238 HVTGFLLALFTHQSWQRCRTISLETGAQNIQMCITMLQLS TCH230
278 PTPEELNVVFTFPLIYS I PQLAFAAI FLG PYVAYKKC - - - ISBT
278 FTAEELVQMLSFPLAYGLFQLIDGPLIVAAYQTYKRRLKN TCH230
315 - HGKNKA - - - EIPESKENGTEPESSFY - - - KANGGPQPDE ISBT
318 KHGKKNSGCTEVCHTRKSTSSRETNAFLEVNEEGAITPGP TCH230
                                                                      ISBT
358 PGPMDCHRALEPVGHITSCE
                                                                      TCH230
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FIG. 2

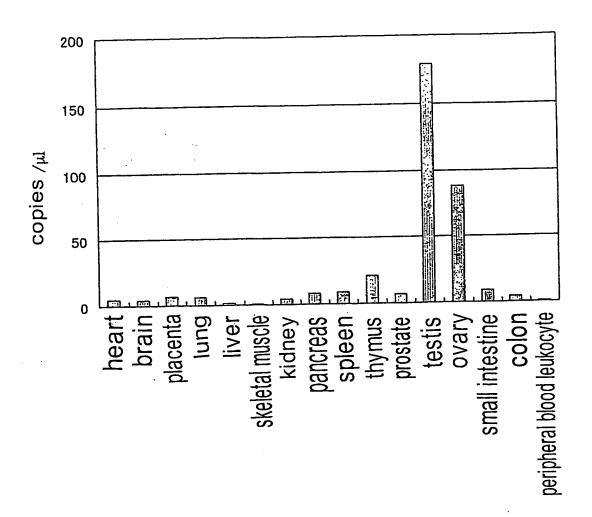
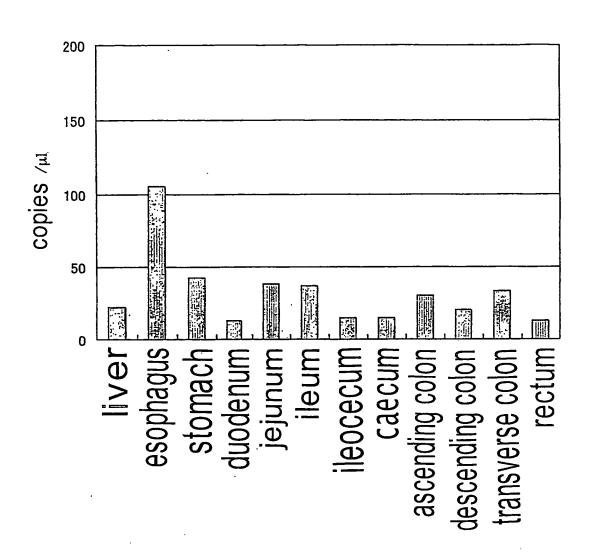


FIG. 3





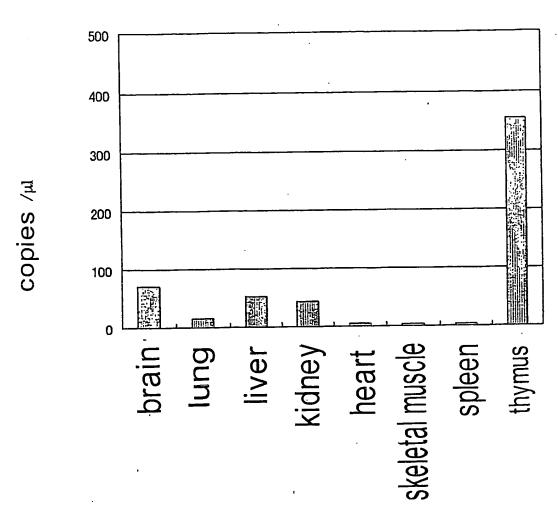
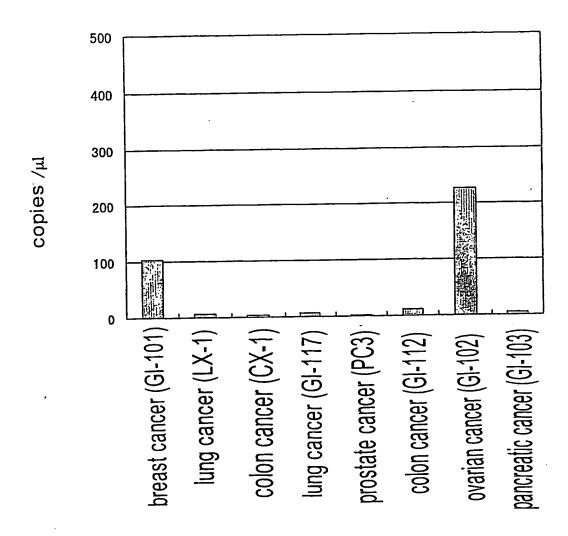


FIG. 5



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TMS TOTAL TOTAL TATA T		CHT PUHT DVPHVOTHEHITLWILLASLAKIGFHLYHKLHTIVPESCLLIMVGLILLGGIIPGVHEKSPHA	135
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FIG. 7

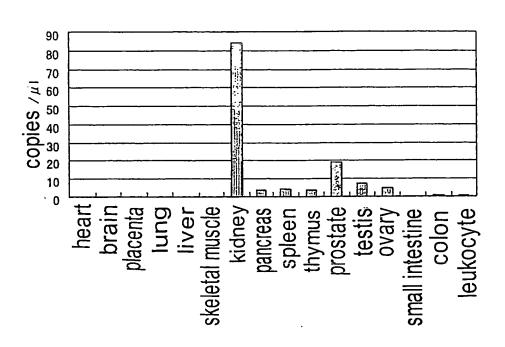


FIG. 8

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FIG. 9

THE HEALT TOT THE BOS TO THE TOTAL T	ALSCKAVICC MATPBA2 ALSCKAVICC MATPBA2 ALSCKAVICC ATPBA1 ALSCKAVICC TCH212 GATMNSDYAT MATPBA2 QAANSSDYST ATPBA1 QAANSSDYST TCH212
F K K C S I A G V T Y G H F P E L A R E Q S S D D F - G R M T S C T N D S C D F N D P R L L K N I E D O F K K C C I A G V A Y G H V P E P B D Y G C S P D E W Q N S Q F G D E K T F S D S S L L E N L D N N I G O F C S I A G V T Y G H F P E L A R E P S S D D F - G R M P P P C S D S C D F D D P R L L K N I E D R N I I I C E F L T M M A V C H T A V P E K D G D E I I Y Q A A S P D E A L V K A A K G L N K L G F V F T G R T P Y S V P I I C E F L T L L A V C H T V V P E K D G D N I I Y Q A A S P D E A L V K A A K G L N F V F T G R T P Y S V P E C I C I Q E F L T L L L A V C H T V V P E K D G D N I I Y Q A S S P D E A L V K A A K G L N F V F T G R T P F S V P E C G D E R Y E L L N V L E F S S D R K R M S V I V R L P S G K L R L Y C K G A D I V I Y D R L A E T S K Y K M E M S V I V N T P S G K L R L Y C K G A D I V I Y D R L A E T S K Y K M E H L E G F A T E G L R T L G F A Y A D L S E N E Y E E M R A V Y O R A S T S V Q N R L L E E C Y E I I E K N H L E Y F A T E G L R T L G F A Y A D L S E N E Y E E W L K V Y O R A S T S V Q N R L L E C Y E I I E K N H L E Y F A T E G L R T L G V A Y A D L S E N E Y E E W L K V Y O R A S T S V Q N R L L E C Y E I I E K N H L E Y F A T E D K L Q D Q V P E T I E T L M K A D I K I M Y L T G D K Q E T A I N I G H S G K L L K K N M G M I T U C A T A I E D K L Q D Q V P E T I E T L M K A D I K I M Y L T G D K Q E T A I N I G H S G K L L K K N M G M I T U C A T A I E D K L Q D Q V P E T I E T L M K A D I K I M Y L T G D K Q E T A I N I G H S G K L L K K N M G M I T U C D M A A L I L C D K A T A I E D K L Q D Q V P E T I E T L M K A D I K I M Y L T G D K Q E T A I N I G H S G K L L K K N M G M I T U C D C C D E T A I N I G H S G K L L K K N M G M I I L C C C C C C C C C C C C C C C C C	GATAIED RLOAGVPETIATLLKAEIRIWVLTGDKGETAINIG YSCRLVSOLSLDATRAAITOHCTDLGNLLKRONDVALIIDGHTLKYALSFEVRRSFLDL SLDATRAAITQHCTDLGNLLGKENDVALIIDGHTLKYALSFEVRRSFLDL SLDATRAAITQHCTTLGDALRKENDFALIIDGHTLKYALSFEVRRSFLDL RVSPLQKSEIVDVKKRVKAITLAIGDGANDVGMIQTAHVGVGISGNEGM RVSPLQKSEIVDVVKKRVKAITLAIGDGANDVGMIQTAHVGVGISGNEGL RVSPLQKSEIVDVVKKRVKAITLAIGDGANDVGMIQTAHVGVGISGNEGL
663 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	

FIG. 10

										•								
	mATP8A2	ATPBAI	TCH212		mATP8A2	ATPBA1	TCHZ12	mATP8A2	ATPBAL	TCH212		ATP8A1 TCH212		matpba2 atpba1	TCH212	MATPBAZ	ATPBA1	TCH212
	VNGFSGQILFERWCIG	NGFSGOILFERWCI	FVNGFSGQILFERWCIG	TM7	TKVFWGHCINALVHSLI	TKVFWVHCLNGLFHSVL	TKVFWGHGINALVHSLI	LETITAWTKFSHLAVWGS	ETSYWTWFSHIAIW	LETTANTKFSHLAVWGS	CLIEDVAWRAAK	VPTA CLIEDV	[[SAKTPPTLFRTGSTQQC FKKNHVNLYRSESLQQN	RKTPPTLFRGSSLQ			
TAS	CILYCFYKNVVLYIIELWFA	CILYCFYKNIVLYIIEIWFA	CILYCFYKNVVLYIIBLWFA		NAEGFN	KENMLKYPELYKTSONALDFN	GEGFN	TIYVVVIVITVCLKAG	NFVYTFVVITVCLKAG	YEFVGNIVYTYVVVTVCLKAGI	KGOATMVLSSAYFWLGLFL	DMSGEAAMLFSSGVFWMGLLF DMRGOATMVLSSAHFWLGLFL		AMERDSNGKRMNBRDRLIKRL VVL GKSLTBRAOLLKNV	RDSNGKRLNERDRLIKRL	X X X X X X X X X X X X X X X X X X X	YDTTKORPDE	AYDTTKKKRK
	FSYLEKLLLVHG	Q F K Y L K N L L M I H G A	AOFSYLEKLL	TW6	YNVIETALPPFTLGIFERSCT	NVMFTAMPPLTIGIFERSCR	PFTLGIFERSCT	WVPMKALEHDTPVTSGHATD	LEWFPLKALQYGTAFGNGKTSD	WFPMKALEHDTVLTSGHATD	S MLIMLVFFGVXSTIWPTIAP	1015 I A L W V V F F G I Y S S L W P A I P M A P D 995 M L T W L V F F G I Y S T I W P T I P I A P I		L L E E V Q E L E T K S R V M G K L V D E V O E L E A K S O D P G A	TOKKTLLEEVQELETKSRVLGK		LLHGYAFSQDENGIVSQSEVIR	VPHGYAFSQEEHGAVSQEEVIR

FIG. 11

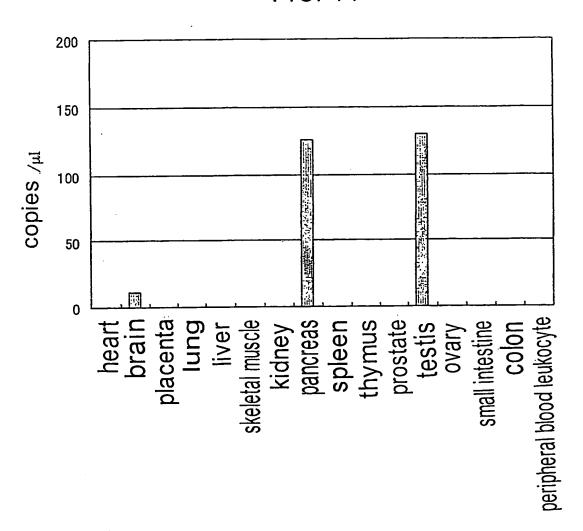
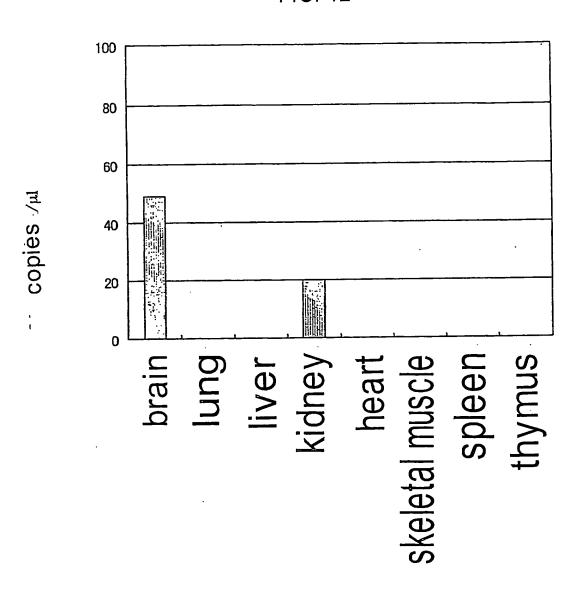
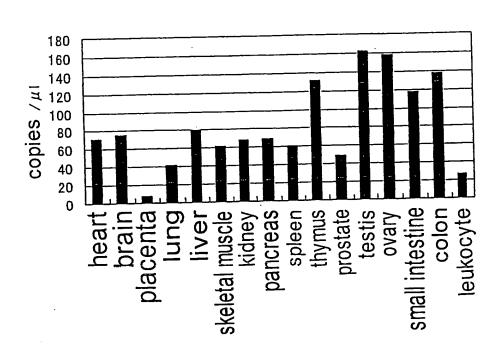


FIG. 12



1 MKKWSSTDLGAAADPLQKDTCPDPLDGDPNSRPPPAKPQLSTAKSRTR hVR1	l
1 MKAHPKEMVPLMGKRVAAPSGNPAVLPEKRPAEITPTKKSAH TCH2	≥00
49 LFGKGDSEEAFPVDCPHEEGELDSCPTITVSPVITIQRPG bVR. 43 FFLEIEGFEPNPTVAKTSPPVFSKPMDSNIROCISGNCDDMDSPQSPQ TCH:	L 2 00
89 DGPTGARLLSQDSVAASTEKTLRLYDRRSIFEAVAQNNCQDLESL hvr. 91 DDVTETPSNPNSPSAQLAKEEQRRKKRRLKKRIFAAVSEGCVEELVEL TCH:	
134 LL FL QK SKKHLTD NEFKDPETGKTCLLKAMLNLHDGQNTT hVR	1 .
139 LV EL QELCRRHDEDVPDFLMHKLTASDTGKTCLMKALLNINPNTKEI TCH	200
174 I PLLLEIAR Q TDSIKELVNASYTDSYYKG Q TALHIA I ERRN MALVTLL bvr	1
187 V RILLAFAE ENDILGRFINAEYTE EAYEG Q TALNIA I ERRQ G D I A ALL TCH	200
222 V E N G A D V Q A A A H G D F F K K T K G R P G F Y F G E L P L S L A A C T N Q L G I V K F L L L VR	1
235 I A A G A D V N A H A K G A P P N P K Y Q H E G F Y F G E T P L A L A A C T N Q P E I V Q L L M TCH	200
270 QNSWQTADISARDSVGNTVLHALVEVADNTADNTKFVTSMYNEILILG hVR	1
283 EH EQTDITSRDSRGNNILHALVTVAEDFKTQNDFVKRMYDMILLRS TCH	200
318 A K L H P T L K L E E L T N K K G M M P L A L A A S T G K I G V L A Y I L O R E I Q E P E C R H hvr	.1
329 G N W E L E T T R N N D G L T P L Q L A A K M G K A E I L K Y I L S R E I K E K R L R S T CH	:200
366 LSRKFTEWAYGPVHSSLYDLSCIDTCEKNSVLEVIAYSSSETPNRHDM hvr	.1
373 LSRKFTDWAYGPVSSSLYDLTNVDTTTDNSVLEITVYNTNID-NRHEM TCH	1200
414 LLVEPLNRLLQDKWDRFVKRIFYFNFLVYCLYMIIFTMAAYYRPVDGL hvr 420 LTLEPLHTLLHMKWKKFAKHMFFLSFCFYFFYNITLTL SYYRPREE - TCH TH2	11 1200
462 PPFKMEKTGDYFRVTGEI - LSVLGGVYFFFRGIQYFLQR hVF 467 EAIPHPLALTHKMGWLQLLGRMFVLIWAMCISVKEGIAIFLLR TCE TH3	1200
500 R P S M K T L F V D S Y S E M L F F L Q S L F M L A T V V L Y F S B L K E Y V A S M V F S L A L bvi 510 P S D L Q S I L S D A W F H F V F F I Q A V L V I L S V F L Y L F A Y K E Y L A C L V L A M A L TCI	1200
548 G W T N M L Y Y T R G F Q Q M G I Y A V M I E K M I L R D L C R F M F V Y I V F L F G F S T A V hVI	R1
558 G W A N M L Y Y T R G F Q S M G M Y S V M I Q K V I L H D V L K F L F V Y I V F L L G F G V A L TCI	H200
596 V TLIED G K N D S L P S E S T S H R W R G P A C R P P D S S Y N S L Y S T C L E L F K F T I DVI	l1
606 A S L I E K C P K D N K D C S S Y G S P S D A V L E L F K L T I TCI	1200
644 GMGDLEFTENYDFKAVFIILLLAYVILTYILLLANDLIALMGETVNKIA hV	R1
638 GLGDLNIQQNSKYPILFLFLLITYVILTFVLLLNMLIALMGETVENVS TC	H200
692 QESKNIWKLQRAITILDTEKSFLKCMRKAFRSGKLLOVGYTPDGKDDY bV	H200
740 RWCFRV DE VNWTTWNTNVGIINED FGN CEGVKRTL SFSLRSSRVSGRH hV. 729 RLCLRINE VKWTEWKTHVSFLNED PGP VRRTADFN TC	
788 WKNFALVPLLREASARDROSAQPEEVYLROFSGSLKPEDAEVFKSPAA bV	R1 H200
836 S G E K	R1
789 T S V .	H200

FIG. 14



```
MRANCSSSSACPANSSEEELPVGLEVHGNLELVFTVVSTV hTCH230
  MSTDCAGNSTCPVNSTEEDPPVGMEGHANLKLLFTVLSAV mTCH230
  MMGLLMFSLGCSVEIRKLWSHIRRPWGIAVGLLCQFGLMP hTCH230
  MVGLVMFSFGCSVESQKLWLHLRRPWGIAVGLLSQFGLMP mTCH230
81 FTAYLLAISFSLKPVQAIAVLIMGCCPGGTISNIFTFWVD hTCH230
81 LTAYLLAIGEGLKPEQAIAVLMMGSCPGGTISNVLTEWVD mTCH230
121 G D M D L S I S M T T C S T V A A L G M M P L C I Y L Y T W S W S L Q Q N L T I hTCH230
121 G D M D L S I S M T T C S T V A A L G M M P L C L Y I Y T R S W T L T Q N L V I mTCH230
161 PYQNIGITLVCLTIPVAFGVYVNYRWPKOSKIILKIGAVV hTCH230
161 PYQSIGITLVSLVVPVASGVYVNYRWPKQATVILKVGAIL mTCH230
201 G G V L L V V A V A G V V L A K G S W N S D I T L L T I S F I F P L I G H V T hTCH230
201 G G M L L L V V A V T G M V L A K G - W N T D V T L L V I S C I F P L V G H V T mTCH230
241 GFLLAL FTHQSWQRCRTISLETGAQNIQMCITMLQLSFTA hTCH230
240 GFLLAFLTHOSWORCRTISIETGAONIOLCIAMLOLSFSA mTCH230
281 EHLVOMLSFPLAYGLFOLIDGFLIVAAYOTYKRRLKNKHG hTCH230
280 EYLVOLLNFALAYGLFQVLHGLLIVAAYQAYKRRQKSKCR mTCH230
321 KKNSGCTEVCHTRKSTSSRETNAFLEVNEEGAITPGPPGP hTCH230
320 RQHPDCPDVCYEKQP---RETSAFLDKGDEAAVTLGPVQP mTCH230
                                                        hTCH230
361 M D CHRALEPVGHITSCE
                                                        mTCH230
357 EQHHRAAELTSHIPSCE
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FIG. 16

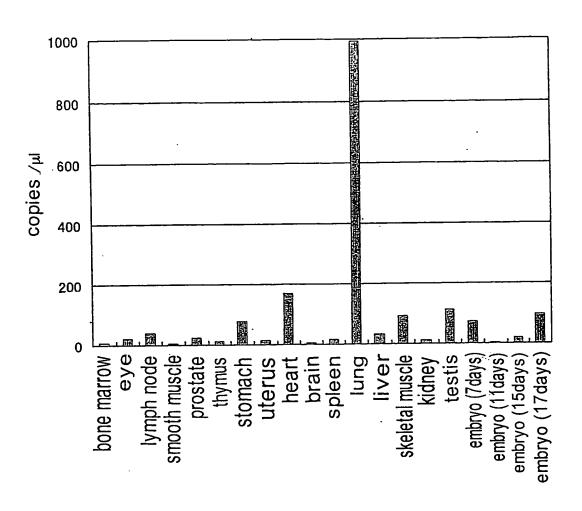


FIG. 17

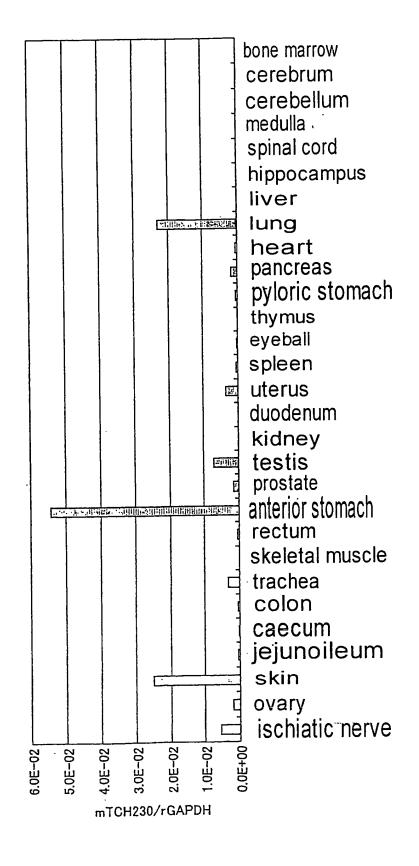


FIG. 18

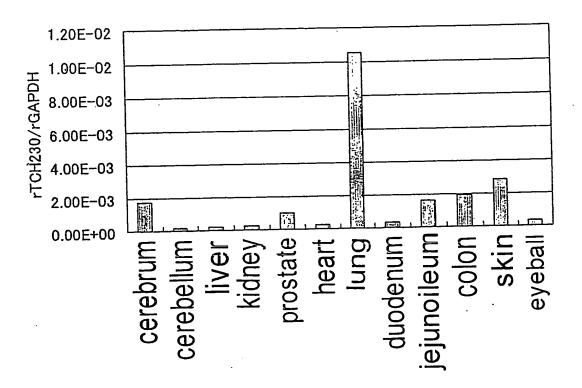


FIG. 19

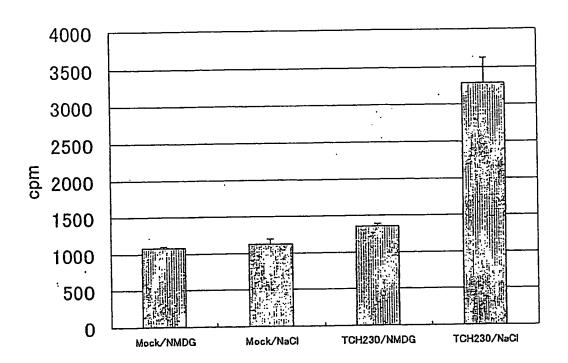


FIG. 20

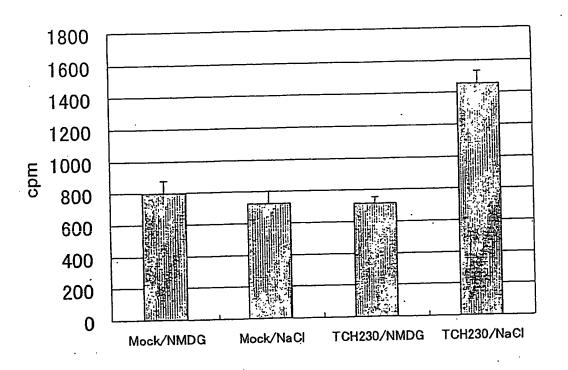


FIG. 21

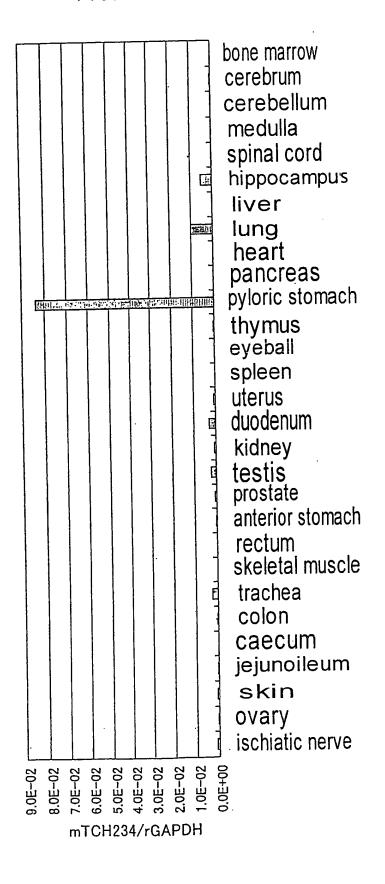


FIG. 22

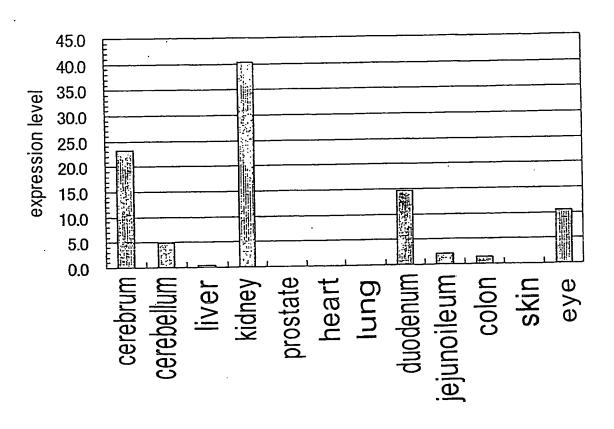


FIG. 23

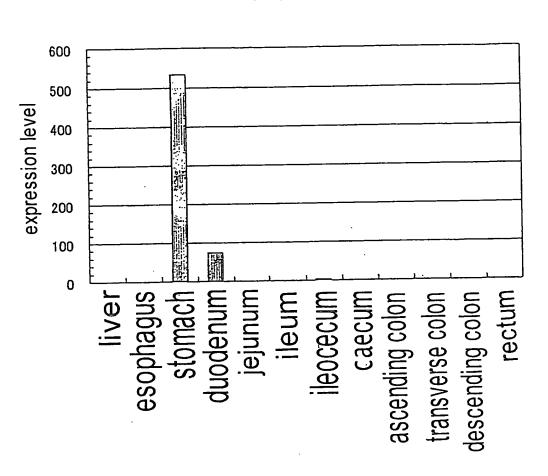


FIG. 24

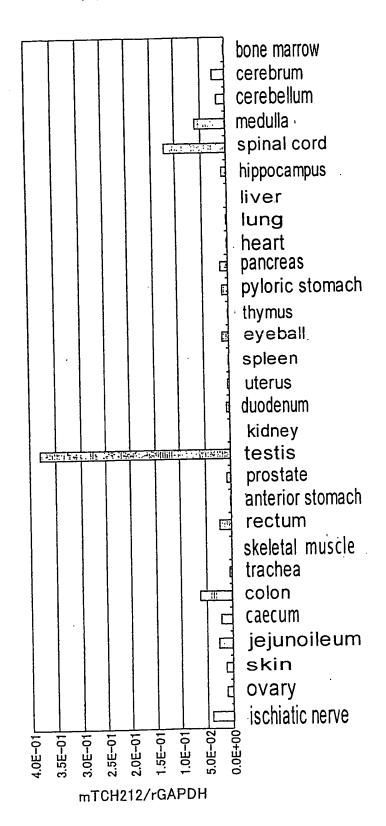


FIG. 25

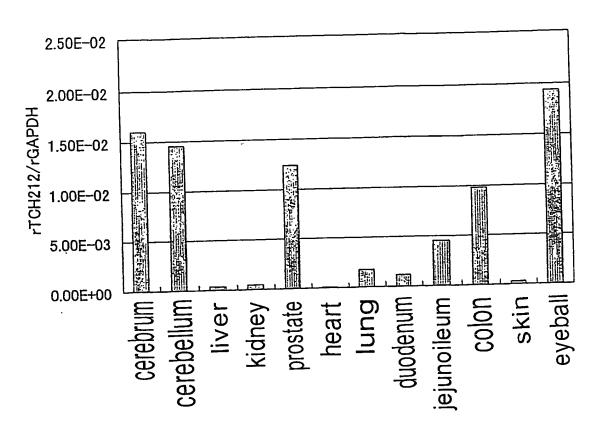


FIG. 26

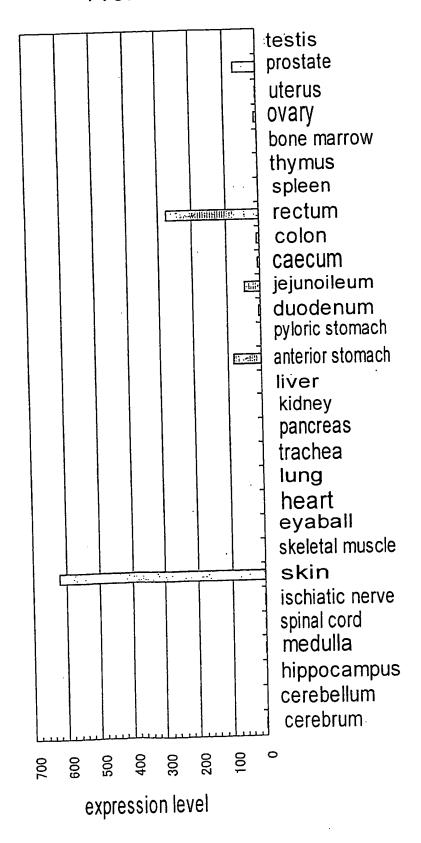


FIG. 27

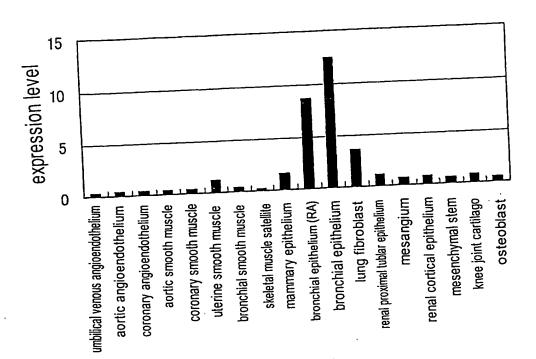


FIG. 28

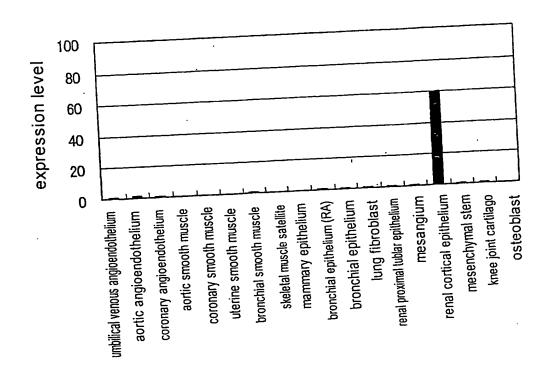


FIG. 29

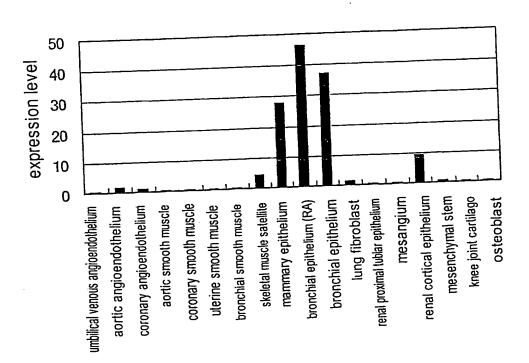


FIG. 30

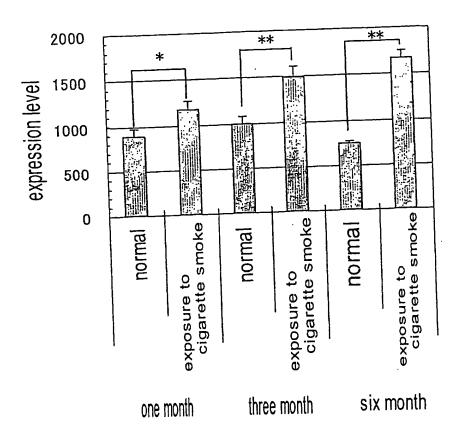


FIG. 31

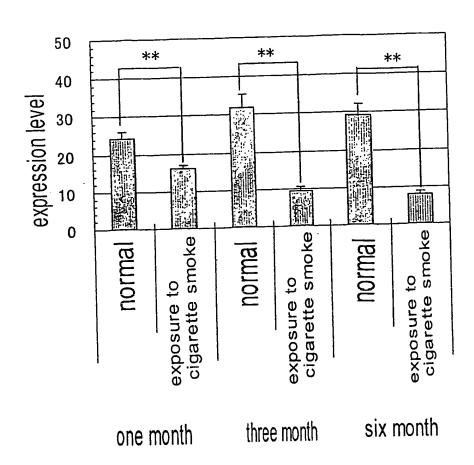


FIG. 32

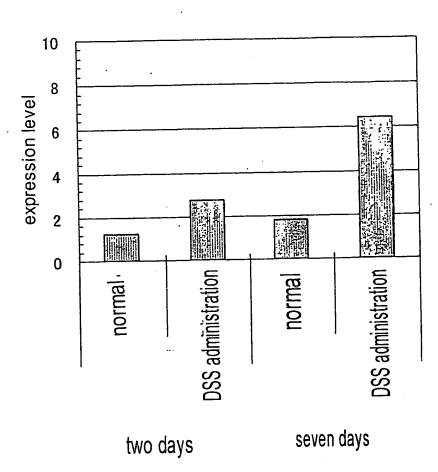


FIG. 33

